

The scores below are sorted by initial score. Significance is calculated based on initial score.

100% identical sequence to the query sequence was not found

3 list of best scores is:

PARAMETERS	
Similarity matrix	PAM-150
Threshold level of sim.	16%
Mismatch penalty	1
Gap penalty	5.00
Gap size penalty	0.05
Window size	90
Cutoff score	1

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	SEARCH	STATISTICS	
Scores :	Mean 59	Median 55	Standard Deviation 6.65
Times :		CPU	Total Elapsed

Number of residues : 4350
 Number of sequences searched : 4
 Number of sequences above cutoff : 1

The scores below are sorted by initial score. Significance is calculated based on initial score.

A 100% [identical] sequence to the query sequence was not found

THE LAST OF THE GREAT

PARAMETERS			
Similarity matrix	PAM	150	K-tuple
Threshold level of sim.	168		
Mismatch penalty	1		Joining penalty
Gap penalty	5.00		Window size
Gap size penalty	0.05		
Cutoff score	1		
Database	2		

SEARCH STATISTICS	
Scores :	Mean 92
Times :	Median 58
	Standard Deviation 35.00
	Total Elapsed 00:00:00
	CPU 00:00:00

Number of residues: 3817
 Number of sequences searched: 5
 Number of scores above cutoff: 5

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The list of best scores is:

PARAMETERS			
Similarity matrix	PAM-150	K-tuple	1
Threshold level of sim.	16%		
Match penalty	1	Joining Penalty	20
Non-matching penalty	1	Constrained	20
Non-matching penalty	1	Joining	20

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SEARCH STATISTICS			
tree:	Mean	Median	Standard Deviation
1	58	55	6.08
2	100.0000	100.0000	0.0000

scores below are sorted by initial score. Significance is calculated based on initial score.

008 Identical sequence to the other sequence was not found

80 PDXAKXYLISIXGLKSVECVRLXGLKSVAFPVDTN 90 SVECVRLXGLKSVAFPVDTN 100 GRIAVRLGVPLQPLPXXQXHX
110 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
120 X 130
PDKAKEYLLSIRGLKSVECVRLTLLHLAGPVDTN 90 GRIAVRLGVPLQPLPXXQXHX
80 90 100 110 X